

C. Saoud

1646 #19

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/469,641B

DATE: 03/27/98
TIME: 14:26:30

INPUT SET: S24473.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: HU, JING-SHAN
6 OLSEN, HENRIK
7 ROSEN, CRAIG G.
8
9 (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING VASCULAR
10 ENDOTHELIAL GROWTH FACTOR 3 POLYPEPTIDES AND METHODS FOR
11 PRODUCING THE POLYPEPTIDES
12
13 (iii) NUMBER OF SEQUENCES: 8
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
17 (B) STREET: 1100 NEW YORK AVE, NW
18 (C) CITY: WASHINGTON
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/469,641
31 (B) FILING DATE: 06-JUN-1995
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: STEFFE, ERIC K.
36 (B) REGISTRATION NUMBER: 36,688
37 (C) REFERENCE/DOCKET NUMBER: 1488.1040000
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-371-2600
41 (B) TELEFAX: 202-371-2540
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47      (A) LENGTH: 666 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: both
50      (D) TOPOLOGY: both
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 1..663
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC      48
63      Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
64          1          5          10          15
65
66      CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG      96
67      Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
68          20          25          30
69
70      AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC      144
71      Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
72          35          40          45
73
74      CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC      192
75      Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
76          50          55          60
77
78      AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC      240
79      Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
80          65          70          75          80
81
82      TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC      288
83      Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
84          85          90          95
85
86      CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG      336
87      Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
88          100          105          110
89
90      ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG      384
91      Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
92          115          120          125
93
94      GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC      432
95      Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
96          130          135          140
97
98      CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA CCC TCC      480
99      Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser

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100	145	150	155	160	
101					
102	CCA GCT GAC ATC ACC CAA TCC CAC TCC AGC CCC AGG CCC CTC TGC CCA				528
103	Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro				
104		165	170	175	
105					
106	CGC TGC ACC CAG CAC CAC CAG TGC CCT GAC CCC CGG ACC TGC CGC TGC				576
107	Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys				
108		180	185	190	
109					
110	CGC TGT CGA CGC CGC AGC TTC CTC CGT TGT CAA GGG CGG GGC TTA GAG				624
111	Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu				
112		195	200	205	
113					
114	CTC AAC CCA GAC ACC TGC AGG TGC CGG AAG CTG CGA AGG TGA				666
115	Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg				
116		210	215	220	
117					
118					
119	(2) INFORMATION FOR SEQ ID NO:2:				
120					
121	(i) SEQUENCE CHARACTERISTICS:				
122	(A) LENGTH: 221 amino acids				
123	(B) TYPE: amino acid				
124	(D) TOPOLOGY: linear				
125					
126	(ii) MOLECULE TYPE: protein				
127					
128	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:				
129					
130	Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val				
131	1	5	10	15	
132					
133	Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg				
134		20	25	30	
135					
136	Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro				
137		35	40	45	
138					
139	Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala				
140		50	55	60	
141					
142	Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys				
143		65	70	75	80
144					
145	Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val				
146		85	90	95	
147					
148	Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu				
149		100	105	110	
150					
151	Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys				
152		115	120	125	

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153
154 Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
155 130 135 140
156
157 Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser
158 145 150 155 160
159
160 Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
161 165 170 175
162
163 Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
164 180 185 190
165
166 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
167 195 200 205
168
169 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
170 210 215 220
171
172

173 (2) INFORMATION FOR SEQ ID NO:3:

174
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 29 base pairs
177 (B) TYPE: nucleic acid
178 (C) STRANDEDNESS: both
179 (D) TOPOLOGY: linear
180

181 (ii) MOLECULE TYPE: cDNA
182
183
184
185

186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

187
188 GCATGGATCC CAGCCTGATG CCCCTGGCC
189

29

190 (2) INFORMATION FOR SEQ ID NO:4:

191
192 (i) SEQUENCE CHARACTERISTICS:
193 (A) LENGTH: 30 base pairs
194 (B) TYPE: nucleic acid
195 (C) STRANDEDNESS: both
196 (D) TOPOLOGY: linear
197

198 (ii) MOLECULE TYPE: cDNA
199
200
201
202

203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

204
205 GCATTCTAGA CCCTGCTGAG TCTGAAAAGC

30

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206

207 (2) INFORMATION FOR SEQ ID NO:5:

208

209 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 29 base pairs

211 (B) TYPE: nucleic acid

212 (C) STRANDEDNESS: both

213 (D) TOPOLOGY: linear

214

215 (ii) MOLECULE TYPE: cDNA

216

217

218

219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

221

222 GACTGCATGC ACCAGAGGAA AGTGGTGTCT

29

223

224 (2) INFORMATION FOR SEQ ID NO:6:

225

226 (i) SEQUENCE CHARACTERISTICS:

227 (A) LENGTH: 29 base pairs

228 (B) TYPE: nucleic acid

229 (C) STRANDEDNESS: both

230 (D) TOPOLOGY: linear

231

232 (ii) MOLECULE TYPE: cDNA

233

234

235

236

237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

238

239 GACTAGATCT CCTTCGCAGC TTCCGGCAC

29

240

241 (2) INFORMATION FOR SEQ ID NO:7:

242

243 (i) SEQUENCE CHARACTERISTICS:

244 (A) LENGTH: 14 amino acids

245 (B) TYPE: amino acid

246 (C) STRANDEDNESS: single

247 (D) TOPOLOGY: Not Relevant

248

249 (ii) MOLECULE TYPE: peptide

250

251

252

253

254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

255

256 Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn

257 1 5 10

258

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SEQUENCE VERIFICATION REPORT
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